



SEQUENCE LISTING

<110> Hoogenboom Hendricus R.J.M.
Hendrik Maria P.G.

<120> MUCIN-1 Specific Binding Members and Methods of Use Thereof

<130> DYX-015.1 US

<140> 09/822,698

<141> 2001-03-30

<150> US 09/538,913

<151> 2000-03-30

<160> 112

<170> Microsoft Word

<210> 1

<211> 113

<212> PRT

<213> artificial sequence

<220>

<223> light chain variable region of the MUC1-specific
binding domain of PH1 Fab antibody

<400> 1

Glu Ile Val Leu Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asn Gly Tyr Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Ser Gly Ser His Arg Ala Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Val Ser Gly Thr Asp Phe Thr Leu Arg Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly
85 90 95

Leu Gln Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105 110

Arg

<210> 2

<211> 339

<212> DNA

<213> artificial sequence

<220>

<223> nucleotide sequence coding for amino acid sequence of
SEQ ID NO:1

<400> 2

gaaattgtgc tgactcagtc tccactctcc ctgcccgtca cccctggaga gccggcctcc 60
atctcctgca ggtctagtca gagcctcctg catagtaatg gatacaccta tttggattgg 120
tacctgcaga agccagggca gtctccacag ctctgatct attcgggttc tcatcgggcc 180
tccgggggtcc ctgacagggt cagtggcagt gtatcaggca cagattttac actgagaatc 240
agcagagtgg aggctgagga tgttgaggtt tattactgca tgcagggtct acagagtcca 300
ttcactttcg gccctgggac caaagtggat atcaaacga 339

<210> 3

<211> 121

<212> PRT

<213> artificial sequence

<220>

<223> heavy chain variable region of the MUC1-specific
binding domain of the PH1 Fab antibody

<400> 3

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Asn
20 25 30
Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Gly Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Tyr Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 4
 <211> 363
 <212> DNA
 <213> artificial sequence

<220>
 <223> nucleotide sequence coding for amino acid sequence of
 SEQ ID NO:3

<400> 4

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tcctgtgcag cctctggatt cacgtttaga agtaacgcca tgggctgggt ccgccaggct      120
ccaggggaagg ggctggagtg ggtctcaggt attagtggta gtggtggcag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgag agccgaggac acggccgtat attattgtgc gaaacatacc      300
ggggggggcg tttgggaccc cattgactac tggggccagg gaaccctggc caccgtctca      360
agc                                                                    363
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<210> 5
 <211> 381
 <212> PRT
 <213> artificial sequence

<220>
 <223> MUC1-specific immunocytokine bivPH1-IL-2

<400> 5

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Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1          5          10          15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Asn
20          25          30
Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35          40          45
Ser Gly Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50          55          60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65          70          75          80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85          90          95
Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Tyr Trp Gly
100         105         110
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Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ala Leu Glu Ile
 115 120 125
 Val Leu Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro
 130 135 140
 Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly
 145 150 155 160
 Tyr Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln
 165 170 175
 Leu Leu Ile Tyr Ser Gly Ser His Arg Ala Ser Gly Val Pro Asp Arg
 180 185 190
 Phe Ser Gly Ser Val Ser Gly Thr Asp Phe Thr Leu Arg Ile Ser Arg
 195 200 205
 Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Leu Gln
 210 215 220
 Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Gly
 225 230 235 240
 Gly Gly Ser Gly Gly Gly Ala Leu Ala Pro Thr Ser Ser Ser Thr Lys
 245 250 255
 Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile
 260 265 270
 Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu
 275 280 285
 Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu
 290 295 300
 Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu
 305 310 315 320
 Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn
 325 330 335
 Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met
 340 345 350
 Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg
 355 360 365
 Trp Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr
 370 375 380

<210> 6
 <211> 1143
 <212> DNA
 <213> artificial sequence

<220>

<223> nucleotide sequence coding for amino acid sequence of
SEQ ID NO:5

<400> 6

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ccaggggaagg ggctggagtg ggtctcaggt attagtggta gtggtggcag cacatactac      180
gcagactccg tgaaggggccg gttcaccatc tccagagaca attccaagaa cacgctgtat      240
ctgcaaataga acagcctgag agccgaggac acggccgtat attattgtgc gaaacataacc      300
ggggggggcg tttgggaccc cattgactac tggggccagg gaaccctggt caccgtctca      360
agcggaggcg gtgcacttga aattgtgctg actcagtcct cactctccct gcccgtcacc      420
cctggagagc cggcctccat ctctgcagg tctagtcaga gcctcctgca tagtaatgga      480
tacacctatt tggattggta cctgcagaag ccagggcagt ctccacagct cctgatctat      540
tcgggttctc atcgggcctc cggggtcctt gacagggtca gtggcagtg atcaggcaca      600
gattttacac tgagaatcag cagagtggag gctgaggatg ttggagtta ttactgcatg      660
cagggctctac agagtccatt cactttcggc cctgggacca aagtggatat caaacgaggg      720
ggtggatcag gcggcggggc cctagcacct acttcaagtt ctacaaagaa aacacageta      780
caactggagc atttactgct ggatttacag atgattttga atggaattaa taattacaag      840
aatcccaaac tcaccaggat gctcacattt aagttttaca tgcccaagaa ggccacagaa      900
ctgaaacatc ttcagtgtct agaagaagaa ctcaaacctc tggaggaagt gctaaattta      960
gctcaaagca aaaactttca cttaagacct agggacttaa tcagcaatat caacgtaata     1020
gttctggaac taaagggatc tgaaacaaca ttcatgtgtg aatatgctga tgagacagca     1080
accattgtag aatttctgaa cagatggatt accttttgtc aaagcatcat ctcaacactg     1140
act                                                                    1143

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<210> 7

<211> 20

<212> PRT

<213> artificial sequence

<220>

<223> peptide of MUC1 protein

<400> 7

Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly
 1 5 10 15
 Ser Thr Ala Pro
 20

<210> 8
 <211> 20
 <212> PRT
 <213> artificial sequence

<220>
 <223> peptide of MUC1 protein

<400> 8

Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro
 1 5 10 15

Pro Ala His Gly
 20

<210> 9
 <211> 24
 <212> DNA
 <213> artificial sequence

<220>
 <223> CH1FOR primer

<400> 9

gtccttgacc aggcagccca gggc 24

<210> 10
 <211> 23
 <212> DNA
 <213> artificial sequence

<220>
 <223> pUC-reverse primer

<400> 10

agcggataac aatttcacac agg 23

<210> 11
 <211> 44
 <212> DNA
 <213> artificial sequence

<220>
 <223> VL backward primer

<400> 11

accgcctcca ccagtgcact tgaaattgtg ctgactcagt ctcc 44

<210> 12

<211> 51

<212> DNA

<213> artificial sequence

<220>

<223> VL forward primer

<400> 12

accgcctcca ccgggcgcg cttattaaca ctctcccctg ttgaagctct t 51

<210> 13

<211> 61

<212> DNA

<213> artificial sequence

<220>

<223> VL backward primer for light chain variable region
of the PH1 Fab antibody with additional linker and
restriction sites

<400> 13

gccgatcgct ctggtcaccg tctcaagcgg aggcggtgca cttgaaattg tgctgactca 60

g 61

<210> 14

<211> 50

<212> DNA

<213> artificial sequence

<220>

<223> VL forward primer for light chain variable region
of PH1 Fab antibody with additional linker and
restriction sites

<400> 14

gtctcgcgag cggccgccga ttggatatcc actttgggtcc cagggccgaa 50

<210> 15

<211> 27

<212> DNA

<213> artificial sequence

<220>

<223> nucleotide sequence coding for a

nine amino acid linker

<400> 15

gggggtggat caggcggcgg ggccta

27

<210> 16

<211> 69

<212> DNA

<213> artificial sequence

<220>

<223> PH1-IL-2 backward primer

<400> 16

accaaagtgg atatcaaacg aggggggtgga tcaggcggcg gggccctagc acctacttca

60

agttctaca

69

<210> 17

<211> 49

<212> DNA

<213> artificial sequence

<220>

<223> PH1-IL-2 forward primer

<400> 17

gtcccgcgtg cggccgcagt cagtgttgag atgatgcttt gacaaaagg

49

<210> 18

<211> 98

<212> PRT

<213> artificial sequence

<220>

<223> heavy chain variable region from a DP47 germ line

<400> 18

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys

<210> 19
<211> 100
<212> PRT
<213> artificial sequence

<220>
<223> light chain variable region from a DPK 15 germ line

<400> 19

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
85 90 95

Leu Gln Thr Pro
100

<210> 20
<211> 14
<212> PRT
<213> artificial sequence

<220>
<223> myc tag peptide

<400> 20

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala
1 5 10

<210> 21
<211> 42

<212> DNA
<213> artificial sequence

<220>
<223> nucleotide sequence coding for amino acid sequence
of SEQ ID NO:20

<400> 21

gaacaaaaac tcatctcaga agaggatctg aatggggccg ca

42

<210> 22
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> hexahistidine peptide

<400> 22

His His His His His His
1 5

<210> 23
<211> 18
<212> DNA
<213> artificial sequence

<220>
<223> nucleotide sequence coding for amino acid sequence
of SEQ ID NO:22

<400> 23

catcaccatc atcaccat

18

<210> 24
<211> 220
<212> PRT
<213> artificial sequence

<220>
<223> immunoglobulin kappa light chain of MUC1-specific PH1-IgG1

<400> 24

Glu Ile Val Leu Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asn Gly Tyr Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser

35	40	45
Pro Gln Leu Leu Ile Tyr Ser Gly Ser His Arg Ala Ser Gly Val Pro		
50	55	60
Asp Arg Phe Ser Gly Ser Val Ser Gly Thr Asp Phe Thr Leu Arg Ile		
65	70	75
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly		
85	90	95
Leu Gln Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys		
100	105	110
Arg Gly Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp		
115	120	125
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn		
130	135	140
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu		
145	150	155
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp		
165	170	175
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr		
180	185	190
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser		
195	200	205
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys		
210	215	220

<210> 25
 <211> 663
 <212> DNA
 <213> artificial sequence

<220>
 <223> nucleotide sequence coding for amino acid sequence of
 SEQ ID NO:24

<400> 25

gaaattgtgc tgactcagtc tccactctcc ctgcccgtca cccctggaga gccggcctcc	60
atctcctgca ggtctagtc gagcctcctg catagtaatg gatacaccta tttggattgg	120
tacctgcaga agccagggca gtctccacag ctctgatct attcgggttc tcatcgggcc	180
tccgggtcc ctgacaggtt cagtggcagt gtatcaggca cagattttac actgagaatc	240
agcagagtgg aggctgagga tgttggagtt tattactgca tgcagggtct acagagtcca	300

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ttcacttttcg gccctgggac caaagtggat atcaaacgag gaactgtggc tgcaccatct 360
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc 420
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccttc 480
caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540
ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600
gaagtcaccc atcagggcct gagttcaccg gtgacaaaaga gcttcaacag gggagagtgt 660
tag 663

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<210> 26
<211> 451
<212> PRT
<213> artificial sequence

<220>
<223> immunoglobulin heavy chain of MUC1-specific PH1-IgG1

<400> 26

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Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Asn
          20          25          30
Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
          35          40          45
Ser Gly Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
          50          55          60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
          65          70          75          80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
          85          90          95
Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Tyr Trp Gly
          100          105          110
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
          115          120          125
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
          130          135          140
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
          145          150          155          160
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
          165          170          175

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[illegible]

<210> 27

<211> 1356
 <212> DNA
 <213> artificial sequence

<220>

<223> nucleotide sequence coding for amino acid sequence of
 SEQ ID NO:26

<400> 27

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tcctgtgcag	cctctggatt	cacgtttaga	agtaacgcca	tgggctgggt	ccgccaggct	120
ccaggggaagg	ggctggagtg	ggtctcaggt	attagtggta	gtgggtggcag	cacatactac	180
gcagactccg	tgaagggccg	gttcaccatc	tccagagaca	attccaagaa	cacgctgtat	240
ctgcaaata	acagcctgag	agccgaggac	acggccgtat	attattgtgc	gaaacatacc	300
ggggggggcg	tttgggaccc	cattgactac	tggggccagg	gaaccctggg	caccgtctca	360
agcgccctcca	ccaagggccc	atcgggtcttc	cccttggcac	cctcctccaa	gagcacctct	420
gggggacacag	cggccctggg	ctgcctggtc	aaggactact	tccccgaacc	ggtgacggtg	480
tcgtggaact	caggcgccct	gaccagcggc	gtccacacct	tcccggtgt	cctacagtcc	540
tcaggactct	actccctcag	cagcgtagtg	accgtgccct	ccagcagctt	gggcacccag	600
acctacatct	gcaacgtgaa	tcacaagccc	agcaacacca	aggtggacaa	gaaagttgag	660
cccaaatactt	gtgacaaaac	tcacacatgc	ccaccgtgcc	cagcacctga	actcctgggg	720
ggaccgtcag	tcttcctctt	ccccccaaaa	ccaagggaca	ccctcatgat	ctccccgacc	780
cctgaggtca	catgcgtggg	ggtggacgtg	agccacgaag	accctgaggt	caagttcaac	840
tggtacgtgg	acggcgtgga	ggtgcataat	gccaagacaa	agccgcggga	ggagcagtac	900
aacagcacgt	accgtgtggg	cagcgtcctc	accgtcctgc	accaggactg	gctgaatggc	960
aaggagtaca	agtgcaagg	ctccaacaaa	gcctcccag	cccccatcga	gaaaaccatc	1020
tccaaagcca	aagggcagcc	ccgagaacca	caggtgtaca	ccctgcccc	atccccggat	1080
gagctgacca	agaaccagg	cagcctgacc	tgcttggtca	aaggcttcta	tcccagcgac	1140
atcgccgtgg	agtgggagag	caatgggcag	ccggagaaca	actacaagac	cacgcctccc	1200
gtgctggact	ccgacggctc	cttcttcttc	tacagcaagc	tcaccgtgga	caagagcagg	1260
tggcagcagg	ggaacgtctt	ctcatgctcc	gtgatgcatg	aggctctgca	caaccactac	1320
acgcagaaga	gcctctcctt	aagtccggga	aaataa			1356

<210> 28
 <211> 14
 <212> PRT
 <213> artificial sequence

 <220>
 <221> variant
 <222> (1)..(14)
 <223> amino acid positions designated Xaa may be varied
 to form alternative regions of a MUC1-specific
 binding member as explained in the disclosure

 <400> 28

Xaa Xaa His Thr Gly Xaa Gly Val Trp Xaa Pro Xaa Xaa Xaa
 1 5 10

<210> 29
 <211> 14
 <212> PRT
 <213> artificial sequence

 <220>
 <223> region of a MUC1-specific binding member

 <400> 29

Ala Lys His Thr Gly Arg Gly Val Trp Asp Pro Ile Gly Tyr
 1 5 10

<210> 30
 <211> 14
 <212> PRT
 <213> artificial sequence

 <220>
 <223> region of a MUC1-specific binding member

 <400> 30

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Lys His
 1 5 10

<210> 31
 <211> 14
 <212> PRT
 <213> artificial sequence

 <220>
 <223> region of a MUC1-specific binding member

 <400> 31

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly Tyr

1

5

10

<210> 32
 <211> 14
 <212> PRT
 <213> artificial sequence

 <220>
 <223> amino acid sequence in a MUC1-specific binding member

 <400> 32

Ala Ile His Thr Gly Gly Gly Val Trp Asp Pro Ile Lys Tyr
 1 5 10

<210> 33
 <211> 33
 <212> DNA
 <213> artificial sequence

 <220>
 <221> misc_feature
 <222> (1)..(33)
 <223> n may be varied according to the disclosure
 to form mutagenic primer sequences

<400> 33
 ggattcacgt ttagannnaa cgccatgggc tgg

33

<210> 34
 <211> 39
 <212> DNA
 <213> artificial sequence

<220>
 <221> misc_feature
 <222> (1)..(39)
 <223> n may be varied according to the disclosure
 to form mutagenic primer sequences

<400> 34
 cacggagtct gcgtannntg tnnngccacc actaccact

39

<210> 35
 <211> 90
 <212> DNA
 <213> artificial sequence

<220>
 <221> misc_feature
 <222> (1)..(90)


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<223>  n may be varied according to the disclosure
        to form mutagenic primer sequences

<400>  35

ctatgagacg gtgaccaggg ttccttgcc ccannnnnnn nnnnnnnnnn nnnnnnnnnn    60
nnnnnnnnnn nnnnnacaat aatatacggc                                     90

<210>  36
<211>  90
<212>  DNA
<213>  artificial sequence

<220>
<221>  misc_feature
<222>  (1)..(90)
<223>  n may be varied according to the disclosure
        to form mutagenic primer sequences

<400>  36

ctatgagacg gtgaccaggg ttccttgcc ccagtagtca atgggggtccc aaacmnnmnn    60
mnnmnnmnnnt ttcgcacaat aatatacggc                                     90

<210>  37
<211>  90
<212>  DNA
<213>  artificial sequence

<220>
<221>  misc_feature
<222>  (1)..(90)
<223>  n may be varied according to the disclosure
        to form mutagenic primer sequences

<400>  37

ctatgagacg gtgaccaggg ttccttgcc ccagtagtcm nnnnnnnnnn nmnnngcccc    60
cccggatatgt ttcgcacaat aatatacggc                                     90

<210>  38
<211>  24
<212>  DNA
<213>  artificial sequence

<220>
<223>  HuJH4-5-FOR primer

<400>  38

tgaggagacg gtgaccaggg ttcc                                     24

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<210> 39
<211> 56
<212> DNA
<213> artificial sequence

<220>
<223> VH1c back Sfi primer

<400> 39

gtcctcgcaa ctgcggccca gccggccatg gccsaggtcc agctggtrca gtctgg 56

<210> 40
<211> 15
<212> PRT
<213> artificial sequence

<220>
<223> PAP peptide epitope of MUC1 bound by PH1 Fab antibody

<400> 40

Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala Leu
1 5 10 15

<210> 41
<211> 16
<212> PRT
<213> artificial sequence

<220>
<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 41

Ala Lys His Asn Thr Ser Lys Val Trp Asp Pro Ile Asp Tyr Trp Gly
1 5 10 15

<210> 42
<211> 48
<212> DNA
<213> artificial sequence

<220>
<223> nucleotide sequence coding for a mutant CDR3 region

<400> 42

gcgaaacata atacgtctaa ggtttgggac cccattgact actggggc 48

<210> 43

<211> 16
 <212> PRT
 <213> artificial sequence

 <220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

 <400> 43

Ala Lys Ser Ser Thr Thr Thr Val Trp Asp Pro Ile Asp Tyr Trp Gly
 1 5 10 15

<210> 44
 <211> 48
 <212> DNA
 <213> artificial sequence

<220>
 <223> nucleotide sequence coding for a mutant CDR3 region

<400> 44

gcgaaatcta gtactacgac ggtttgggac cccattgact actggggc

48

<210> 45
 <211> 16
 <212> PRT
 <213> artificial sequence

<220>
 <221> variant
 <222> (1)..(16)
 <223> Xaa, designated as "&" in the disclosure, indicates end
 of amino acid sequence because mutation in nucleotide
 sequence forms a translational stop codon

<400> 45

Ala Lys Xaa Pro Met Ala Asn Val Trp Asp Pro Ile Asp Tyr Trp Gly
 1 5 10 15

<210> 46
 <211> 48
 <212> DNA
 <213> artificial sequence

<220>
 <223> nucleotide sequence coding for a mutant CDR3 region

<400> 46

gcgaaatagc ctatggcgaa tgtttgggac cccattgact actggggc

48

<210> 47
 <211> 16
 <212> PRT
 <213> artificial sequence

 <220>
 <221> variant
 <222> (1)..(16)
 <223> Xaa, designated as "&" in the disclosure, indicates end
 of amino acid sequence because mutation in nucleotide
 sequence forms a translational stop codon

 <400> 47

 Ala Lys Xaa His Thr Lys Thr Val Trp Asp Pro Ile Asp Tyr Trp Gly
 1 5 10 15

<210> 48
 <211> 48
 <212> DNA
 <213> artificial sequence

 <220>
 <223> nucleotide sequence coding for a mutant CDR3 region

 <400> 48

gcgaaatagc atacgaagac ggtttgggac cccattgact actggggc 48

<210> 49
 <211> 16
 <212> PRT
 <213> artificial sequence

 <220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

 <400> 49

Ala Lys Ile Thr Val Ser Arg Val Trp Asp Pro Ile Asp Tyr Trp Gly
 1 5 10 15

<210> 50
 <211> 48
 <212> DNA
 <213> artificial sequence

 <220>
 <223> nucleotide sequence coding for a mutant CDR3 region

 <400> 50

gcgaaaatta ctgttagtcg tgtttgggac cccattgact actggggc 48

<210> 51
 <211> 16
 <212> PRT
 <213> artificial sequence

 <220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

 <400> 51

Ala	Lys	Arg	Tyr	Leu	Tyr	Asp	Val	Trp	Asp	Pro	Ile	Asp	Tyr	Trp	Gly
1				5				10						15	

<210> 52
 <211> 48
 <212> DNA
 <213> artificial sequence

 <220>
 <223> nucleotide sequence coding for a mutant CDR3 region

 <400> 52

gcgaaacggt atctgtatga tgtttgggac cccattgact actggggc 48

<210> 53
 <211> 16
 <212> PRT
 <213> artificial sequence

 <220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

 <400> 53

Ala	Lys	His	Thr	Gly	Gly	Gly	Thr	Leu	Gln	Arg	Leu	Asp	Tyr	Trp	Gly
1				5				10						15	

<210> 54
 <211> 48
 <212> DNA
 <213> artificial sequence

 <220>
 <223> nucleotide sequence coding for a mutant CDR3 region

 <400> 54

gcgaaacata ccgggggggg cactttgcag cggttgact actggggc 48

<210> 55
 <211> 16

<212> PRT
 <213> artificial sequence

 <220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

 <400> 55

Ala	Lys	His	Thr	Gly	Gly	Gly	Thr	Gln	Thr	Pro	Cys	Asp	Tyr	Trp	Gly
1				5				10						15	

<210> 56
 <211> 48
 <212> DNA
 <213> artificial sequence

 <220>
 <223> nucleotide sequence coding for a mutant CDR3 region

 <400> 56

gcgaaacata ccggggggggg cactcagact ccgtgtgact actgggggc 48

<210> 57
 <211> 16
 <212> PRT
 <213> artificial sequence

 <220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

 <400> 57

Ala	Lys	His	Thr	Gly	Gly	Gly	Arg	Arg	Ile	Cys	His	Asp	Tyr	Trp	Gly
1				5				10						15	

<210> 58
 <211> 48
 <212> DNA
 <213> artificial sequence

 <220>
 <223> nucleotide sequence coding for a mutant CDR3 region

 <400> 58

gcgaaacata ccggggggggg ccgtcgtatt tgtcatgact actgggggc 48

<210> 59
 <211> 16
 <212> PRT
 <213> artificial sequence

<220>
 <221> variant
 <222> (1)..(16)
 <223> Xaa, designated as "&" in the disclosure, indicates end
 of amino acid sequence because mutation in nucleotide
 sequence forms a translational stop codon

<400> 59

Ala	Lys	His	Thr	Gly	Gly	Gly	Xaa	Arg	Xaa	Xaa	Arg	Asp	Tyr	Trp	Gly
1				5				10						15	

<210> 60
 <211> 48
 <212> DNA
 <213> artificial sequence

<220>
 <223> nucleotide sequence coding for a mutant CDR3 region

<400> 60

gcgaaacata ccgsgggggggg ctagcggtag tagcgggact actggggc

48

<210> 61
 <211> 16
 <212> PRT
 <213> artificial sequence

<220>
 <223> mutant CDR3 region of an antibody heavychain variable region

<400> 61

Ala	Lys	His	Thr	Gly	Gly	Gly	Gln	Lys	Leu	Gln	Leu	Asp	Tyr	Trp	Gly
1				5				10						15	

<210> 62
 <211> 48
 <212> DNA
 <213> artificial sequence

<220>
 <223> nucleotide sequence coding for a mutant CDR3 region

<400> 62

gcgaaacata ccgsgggggggg ccagaagctg cagctggact actggggc

48

<210> 63
 <211> 16
 <212> PRT
 <213> artificial sequence

<220>
 <221> variant
 <222> (1)..(16)
 <223> Xaa, when designated as "&" in the disclosure, indicates end of amino acid sequence because mutation in nucleotide sequence forms a translational stop codon; or when designated as "s" in the disclosure, Xaa is serine

<400> 63

Ala	Xaa	His	Thr	Gly	Gly	Arg	Gly	Trp	Asp	Pro	Ile	Asp	Tyr	Trp	Gly
1				5				10						15	

<210> 64
 <211> 48
 <212> DNA
 <213> artificial sequence

<220>
 <223> nucleotide sequence coding for a mutant CDR3 region

<400> 64

gcgtsacata cggggggggcg cggttgggac cccattgact actggggc 48

<210> 65
 <211> 16
 <212> PRT
 <213> artificial sequence

<220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

<400> 65

Ala	Asn	Gln	Thr	Gly	Gly	Gly	Val	Trp	Asp	Pro	Ile	Asp	Tyr	Trp	Gly
1				5				10						15	

<210> 66
 <211> 48
 <212> DNA
 <213> artificial sequence

<220>
 <223> nucleotide sequence coding for a mutant CDR3 region

<400> 66

gcgaaccaga ctggggggggg cgtttgggac cccattgact actggggc 48

<210> 67
 <211> 16

<212> PRT
 <213> artificial sequence

 <220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

 <400> 67

Ala Arg His Thr Gly Gly Gly Val Trp Asp Pro Ile Tyr Tyr Trp Gly
 1 5 10 15

<210> 68
 <211> 48
 <212> DNA
 <213> artificial sequence

<220>
 <223> nucleotide sequence coding for a mutant CDR3 region

<400> 68

gcgagacata ccggtggggg cgtktgggat cccatatact actggggc

48

<210> 69
 <211> 16
 <212> PRT
 <213> artificial sequence

<220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

<400> 69

Ala Lys Pro Thr Gly Gly Gly Ala Trp Asp Pro Ile Asp Tyr Trp Gly
 1 5 10 15

<210> 70
 <211> 48
 <212> DNA
 <213> artificial sequence

<220>
 <223> nucleotide sequence coding for a mutant CDR3 region

<400> 70

gcgaaacctt ccgggggggg cgcttgggac cccattgact actggggc

48

<210> 71
 <211> 16
 <212> PRT
 <213> artificial sequence

<220>
<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 71

Ala Lys His Thr Gly Val Gly Val Trp His Pro Ile Tyr Tyr Trp Gly
1 5 10 15

<210> 72
<211> 48
<212> DNA
<213> artificial sequence

<220>
<223> nucleotide sequence coding for a mutant CDR3 region

<400> 72

gcgaaacata ccgggggtggg cgtttggcac cccatctact actgggggc 48

<210> 73
<211> 14
<212> PRT
<213> artificial sequence

<220>
<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 73

Ala Lys His Thr Gly Val Gly Val Trp Asp Pro Ile Lys Tyr
1 5 10

<210> 74
<211> 14
<212> PRT
<213> artificial sequence

<220>
<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 74

Ala Lys His Thr Gly Glu Gly Val Trp Asp Pro Ile Lys Tyr
1 5 10

<210> 75
<211> 14
<212> PRT
<213> artificial sequence

<220>
<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 75

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Lys
1 5 10

<210> 76

<211> 14

<212> PRT

<213> artificial sequence

<220>

<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 76

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly Tyr
1 5 10

<210> 77

<211> 14

<212> PRT

<213> artificial sequence

<220>

<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 77

Ala Arg His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly Tyr
1 5 10

<210> 78

<211> 14

<212> PRT

<213> artificial sequence

<220>

<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 78

Ser Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly Tyr
1 5 10

<210> 79

<211> 14

<212> PRT

<213> artificial sequence

<220>

<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 79

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly His
1 5 10

<210> 80

<211> 14

<212> PRT

<213> artificial sequence

<220>

<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 80

Ala Lys His Thr Gly Gly Gly Val Trp Asn Pro Ile Gly His
1 5 10

<210> 81

<211> 14

<212> PRT

<213> artificial sequence

<220>

<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 81

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Leu Gly Tyr
1 5 10

<210> 82

<211> 14

<212> PRT

<213> artificial sequence

<220>

<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 82

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Leu Asp Asn
1 5 10

<210> 83

<211> 14

<212> PRT

<213> artificial sequence

<220>

<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 83

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asn Tyr
1 5 10

<210> 84

<211> 14

<212> PRT

<213> artificial sequence

<220>

<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 84

Ala Arg His Thr Gly Gly Gly Val Trp Asp Pro Ile Asn Tyr
1 5 10

<210> 85

<211> 14

<212> PRT

<213> artificial sequence

<220>

<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 85

Ala Lys His Thr Gly Ser Gly Val Trp Asp Pro Ile Asn Tyr
1 5 10

<210> 86

<211> 14

<212> PRT

<213> artificial sequence

<220>

<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 86

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asn Asp
1 5 10

<210> 87

<211> 14

<212> PRT

<213> artificial sequence

<220>

<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 87

Ala Lys His Thr Gly Val Gly Val Trp Asp Pro Met Asn Tyr
 1 5 10

<210> 88
 <211> 14
 <212> PRT
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<220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

<400> 88

Thr Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asn Tyr
 1 5 10

<210> 89
 <211> 14
 <212> PRT
 <213> artificial sequence

<220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

<400> 89

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Ala Tyr
 1 5 10

<210> 90
 <211> 14
 <212> PRT
 <213> artificial sequence

<220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

<400> 90

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Ala Asn
 1 5 10

<210> 91
 <211> 14
 <212> PRT
 <213> artificial sequence

<220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

<400> 91

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Phe Ala Tyr

1 5 10

<210> 92
<211> 14
<212> PRT
<213> artificial sequence

<220>
<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 92

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Met Ala Ser
1 5 10

<210> 93
<211> 14
<212> PRT
<213> artificial sequence

<220>
<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 93

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Met Asp Tyr
1 5 10

<210> 94
<211> 14
<212> PRT
<213> artificial sequence

<220>
<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 94

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile His Tyr
1 5 10

<210> 95
<211> 14
<212> PRT
<213> artificial sequence

<220>
<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 95

Ala Ile His Thr Gly Ala Gly Val Trp Asp Pro Ile Arg Tyr
1 5 10

<210> 96
<211> 14
<212> PRT
<213> artificial sequence

<220>
<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 96

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Ser Ser
1 5 10

<210> 97
<211> 14
<212> PRT
<213> artificial sequence

<220>
<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 97

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Asp
1 5 10

<210> 98
<211> 14
<212> PRT
<213> artificial sequence

<220>
<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 98

Val Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Val Tyr
1 5 10

<210> 99
<211> 14
<212> PRT
<213> artificial sequence

<220>
<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 99

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Val Asp Tyr
1 5 10

<210> 100
 <211> 14
 <212> PRT
 <213> artificial sequence

 <220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

 <400> 100

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Val Pro
 1 5 10

<210> 101
 <211> 14
 <212> PRT
 <213> artificial sequence

<220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

 <400> 101

Val Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Ala Tyr
 1 5 10

<210> 102
 <211> 14
 <212> PRT
 <213> artificial sequence

<220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

 <400> 102

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile His Asn
 1 5 10

<210> 103
 <211> 14
 <212> PRT
 <213> artificial sequence

<220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

 <400> 103

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Met His Tyr
 1 5 10

<210> 104
 <211> 14

<212> PRT
 <213> artificial sequence

 <220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

 <400> 104

Ala Lys His Thr Gly Gly Gly Val Trp Asn Pro Ile Asp Tyr
 1 5 10

<210> 105
 <211> 14
 <212> PRT
 <213> artificial sequence

<220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

 <400> 105

Val Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Tyr
 1 5 10

<210> 106
 <211> 14
 <212> PRT
 <213> artificial sequence

<220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

 <400> 106

Ala Lys His Thr Gly Ala Gly Val Trp Asp Pro Ile Asp Tyr
 1 5 10

<210> 107
 <211> 14
 <212> PRT
 <213> artificial sequence

<220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

 <400> 107

Ala Gln His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly Tyr
 1 5 10

<210> 108
 <211> 14
 <212> PRT

<213> artificial sequence

<220>

<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 108

Ala Lys His Thr Gly Arg Gly Val Trp Asp Pro Ile Asp Tyr
1 5 10

<210> 109

<211> 14

<212> PRT

<213> artificial sequence

<220>

<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 109

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Tyr Tyr
1 5 10

<210> 110

<211> 66

<212> DNA

<213> artificial sequence

<220>

<223> VH1C Back eukaryotic primer

<400> 110

ggactagtc tggagtgcgc gcactcccag gtccagctgg tgcagtctgg gggaggcttg 60

gtacag 66

<210> 111

<211> 73

<212> DNA

<213> artificial sequence

<220>

<223> VKexpress-MUC-for primer

<400> 111

gcgctcgcat ttgcctgtta attaagttag atctattcta ctcaagtttg atatccactt 60

tggtcccagg gcc 73

<210> 112

<211> 35

<212> DNA

<213> artificial sequence

<220>

<223> MUC1-VL-Back-APA primer

<400> 112

ccagtgcact ccgaaattgt gctgactcag tctcc

35

[illegible]